



App. No. 09/438,185

Response to Office communication dated 09/03/2003

Office communication of July 8, 2003

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PATENT

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Replacement Pages to the Specification:

Please replace pages 37 and 123 with the following replacement pages, together with annotated sheets showing changes in highlights. The replacement pages and annotated pages are attached to this amendment.

Attachment: Replacement Sheets
Annotated Sheets Showing Changes

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tRNAs

| <u>tRNA #</u> | <u>Begin</u> | <u>End</u> | <u>Type</u> | <u>Codon</u> |
|---------------|--------------|------------|-------------|--------------|
| 1 | 89657 | 89728 | Thr | GGT |
| 2 | 90998 | 91070 | Trp | CCA |
| 3 | 199301 | 199229 | Met | CAT |
| 4 | 199390 | 199317 | Met | CAT |
| 5 | 296075 | 296147 | Val | TAC |
| 6 | 296151 | 296224 | Asp | GTC |
| 7 | 409848 | 409922 | Pro | TGG |
| 8 | 462141 | 462214 | Arg | CCT |
| 9 | 672236 | 672318 | Leu | CAA |
| 10 | 677264 | 677337 | Arg | TCG |
| 11 | 739403 | 739486 | Leu | CAG |
| 12 | 781610 | 781680 | Gly | TCC |
| 13 | 784822 | 784896 | Glu | TTC |
| 14 | 784922 | 784994 | Lys | TTT |
| 15 | 836119 | 836191 | Ala | GGC |
| 16 | 843926 | 843999 | Pro | GGG |
| 17 | 877400 | 877473 | Arg | ACG |
| 18 | 1085605 | 1085676 | Gln | TTG |
| 19 | 1142034 | 1142118 | Ser | TGA |
| 20 | 1175863 | 1175944 | Leu | TAG |
| 21 | 1230028 | 1229942 | Ser | CGA |
| 22 | 1137462 | 1137389 | Val | GAC |
| 23 | 1030603 | 1030533 | Cys | GCA |
| 24 | 1000022 | 999949 | His | GTG |
| 25 | 961607 | 961536 | Gly | GCC |
| 26 | 807413 | 807341 | Arg | TCT |
| 27 | 786780 | 786708 | Thr | CGT |
| 28 | 715971 | 715889 | Leu | TAA |
| 29 | 708441 | 708354 | Ser | GCT |
| 30 | 680259 | 680178 | Leu | GAG |
| | 631445 | 631373 | Phe | GAA |
| 32 | 626987 | 626901 | Ser | GGA |
| 33 | 293477 | 293405 | Thr | TGT |
| 34 | 293399 | 293317 | Tyr | GTA |
| 35 | 269142 | 269070 | Ala | TGC |
| 36 | 269065 | 268992 | Ile | GAT |
| 37 | 1643089 | 164318 | Asn | GTT |
| 38 | 87522 | 87450 | Met | CAT |



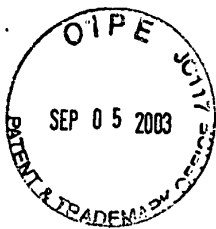
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TABLE 2

| Gene # | From | To | Strand | Gene Function (C. Trachomatis Ortholog in parenthesis) |
|---------|-------|-------|--------|---|
| CPn0001 | 282 | 4 | R | CT001 hypothetical protein |
| CPn0002 | 573 | 875 | F | gatC-Glu-tRNA Gln Amidotransferase (C subunit) - (CT002) |
| CPn0003 | 895 | 2370 | F | gatA-Glu tRNA Gln Amidotransferase-(CT003) |
| CPn0004 | 2370 | 3833 | F | gatB-(Pet 112) Glu tRNA Gln Amidotransferase (B Subunit) |
| CPn005 | 4127 | 6892 | F | pmp_1-Polymorphic Outer Membrane Protein G Family |
| CPn006 | 7293 | 7141 | R | |
| CPn007 | 7605 | 10496 | F | |
| CPn008 | 10975 | 11685 | F | |
| CPn009 | 11815 | 13119 | F | |
| CPn0010 | 13435 | 14325 | F | |
| CPn0010 | 14379 | 15746 | F | frame-shift with 0010 |
| CPn0011 | 15892 | 16614 | F | |
| CPn0012 | 16644 | 18212 | F | |
| CPn0013 | 18584 | 21106 | F | pmp_2-Polymorphic Outer Membrane Protein G Family |
| CPn0014 | 21392 | 21922 | F | pmp_3-Polymorphic Outer Membrane Protein G Family |
| CPn0015 | 21835 | 24174 | F | pmp_3-PMP_3 (frame-shift with 0014) |
| CPn0016 | 24416 | 26188 | F | pmp_4-Polymorphic Outer Membrane Protein G Family |
| CPn0017 | 26094 | 27170 | F | pmp_4-PMP_4 (frame-shift with 0016) |
| CPn0018 | 27522 | 29003 | F | pmp_5-Polymorphic Outer Membrane Protein G Family |
| CPn0019 | 29007 | 30356 | F | pmp_5-PMP_5 (frame-shift with 0018) |
| CPn0020 | 32687 | 30603 | R | Predicted OMP [leader (14) peptide: outer membrane] - (CT351) |
| CPn0021 | 34410 | 32707 | R | Predicted OMP [leader (19) peptide] - (CT350) |
| CPn0022 | 34982 | 34395 | R | maf-(CT349) |
| CPn0023 | 36603 | 35014 | R | yjK/alr-ABC Transporter Protein ATPase-(CT348) |
| CPn0024 | 37596 | 36661 | R | xerC-Integrase/recombinase-(CT347) |
| CPn0025 | 38604 | 37684 | R | elaC/atsA-Sulphohydrolase/Glycosulfatase-(CT346) |
| CPn0026 | 39625 | 38762 | R | CT345 hypothetical protein-(CT345) |
| CPn0027 | 42234 | 39778 | R | lon-Lon ATP-dependent Protease-(CT344) |
| CPn0028 | 43325 | 42543 | R | |
| CPn0029 | 43755 | 43390 | R | |
| CPn0030 | 43891 | 44529 | F | gcp_1-O-Sialoglycoprotein Endopeptidase_1-(CT343) |
| CPn0031 | 44711 | 44884 | F | rs21-S21 Ribosomal Protein-(CT342) |
| CPn0032 | 44923 | 46098 | F | dnaJ-Heat Shock Protein J-(CT341) |
| CPn0033 | 46138 | 48171 | F | pdhA&B/odbA&odbB-(pyruvate) Oxoisovalerate Dehydrogenase Alpha & ___ Fusion-(CT340) |
| CPn0034 | 49457 | 48210 | R | |
| CPn0035 | 51029 | 49569 | R | CT339 hypothetical protein |
| CPn0036 | 51002 | 51796 | F | CT338 hypothetical protein |
| CPn0037 | 51792 | 52115 | F | ptsH-PTS Phosphocarrier Protein Hpr-(CT337) |
| CPn0038 | 52119 | 53831 | F | ptsI-PTS PEP Phosphotransferase-(CT336) |
| CPn0039 | 54250 | 53963 | R | ybaB-(CT335) |



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TABLE 2

| Gene # | From | To | Strand | Gene Function (C. Trachomatis Ortholog in parenthesis) |
|---------|-------|-------|--------|---|
| CPn0001 | 282 | 4 | R | CT001 hypothetical protein |
| CPn0002 | 573 | 875 | F | gatC-Glu-tRNA Gln Amidotransferase (C subunit) - (CT002) |
| CPn0003 | 895 | 2370 | F | gatA-Glu tRNA Gln Amidotransferase-(CT003) |
| CPn0004 | 2370 | 3833 | F | gatB-(Pet 112) Glu tRNA Gln Amidotransferase (B Subunit) |
| CPn0005 | 4127 | 6892 | F | pmp_1-Polymorphic Outer Membrane Protein G Family |
| CPn0006 | 7293 | 7141 | R | |
| CPn0007 | 7605 | 10496 | F | |
| CPn0008 | 10975 | 11685 | F | |
| CPn0009 | 11815 | 13119 | F | |
| CPn0010 | 13435 | 14325 | F | |
| CPn0010 | 14379 | 15746 | F | frame-shift with 0010 |
| CPn0011 | 15892 | 16614 | F | |
| CPn0012 | 16644 | 18212 | F | |
| CPn0013 | 18584 | 21106 | F | pmp_2-Polymorphic Outer Membrane Protein G Family |
| CPn0014 | 21392 | 21922 | F | pmp_3-Polymorphic Outer Membrane Protein G Family |
| CPn0015 | 21835 | 24174 | F | pmp_3-PMP_3 (frame-shift with 0014) |
| CPn0016 | 24416 | 26188 | F | pmp_4-Polymorphic Outer Membrane Protein G Family |
| CPn0017 | 26094 | 27170 | F | pmp_4-PMP_4 (frame-shift with 0016) |
| CPn0018 | 27522 | 29003 | F | pmp_5-Polymorphic Outer Membrane Protein G Family |
| CPn0019 | 29007 | 30356 | F | pmp_5-PMP_5 (frame-shift with 0018) |
| CPn0020 | 32687 | 30603 | R | Predicted OMP [leader (14) peptide: outer membrane] - (CT351) |
| CPn0021 | 34410 | 32707 | R | Predicted OMP [leader (19) peptide] - (CT350) |
| CPn0022 | 34982 | 34395 | R | maf-(CT349) |
| CPn0023 | 36603 | 35014 | R | yjK/alr-ABC Transporter Protein ATPase-(CT348) |
| CPn0024 | 37596 | 36661 | R | xerC-Integrase/recombinase-(CT347) |
| CPn0025 | 38604 | 37684 | R | elaC/atsA-Sulphohydrolase/Glycosulfatase-(CT346) |
| CPn0026 | 39625 | 38762 | R | CT345 hypothetical protein-(CT345) |
| CPn0027 | 42234 | 39778 | R | lon-Lon ATP-dependent Protease-(CT344) |
| CPn0028 | 43325 | 42543 | R | |
| CPn0029 | 43755 | 43390 | R | |
| CPn0030 | 43891 | 44529 | F | gcp_1-O-Sialoglycoprotein Endopeptidase_1-(CT343) |
| CPn0031 | 44711 | 44884 | F | rs21-S21 Ribosomal Protein-(CT342) |
| CPn0032 | 44923 | 46098 | F | dnaJ-Heat Shock Protein J-(CT341) |
| CPn0033 | 46138 | 48171 | F | pdhA&B/odbA&odbB-(pyruvate) Oxoisovalerate Dehydrogenase Alpha & ___ Fusion-(CT340) |
| CPn0034 | 49457 | 48210 | R | |
| CPn0035 | 51029 | 49569 | R | CT339 hypothetical protein |
| CPn0036 | 51002 | 51796 | F | CT338 hypothetical protein |
| CPn0037 | 51792 | 52115 | F | ptsH-PTS Phosphocarrier Protein Hpr-(CT337) |
| CPn0038 | 52119 | 53831 | F | ptsI-PTS PEP Phosphotransferase-(CT336) |
| CPn0039 | 54250 | 53963 | R | ybaB-(CT335) |



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cRNAs

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| cRNA # | Begin | End | Type | Codon |
|--------|---------|---------|------|-------|
| 1 | 89657 | 89728 | Thr | GGT |
| 2 | 90998 | 91070 | Trp | GCA |
| 3 | 100000 | 100001 | Met | CAT |
| 4 | 100017 | 100000 | Met | CAT |
| 5 | 296075 | 296147 | Val | TAC |
| 6 | 296151 | 296224 | Asp | GTC |
| 7 | 409848 | 409922 | Pro | TGG |
| 8 | 462141 | 462214 | Arg | CCT |
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| 10 | 677264 | 677337 | Arg | TCG |
| 11 | 739403 | 739486 | Leu | CAG |
| 12 | 781610 | 781680 | Gly | TCC |
| 13 | 784822 | 784896 | Glu | TTC |
| 14 | 784922 | 784994 | Lys | TTT |
| 15 | 836119 | 836191 | Ala | GGC |
| 16 | 843926 | 843999 | Pro | GGG |
| 17 | 877400 | 877473 | Arg | ACG |
| 18 | 1085605 | 1085676 | Gln | TTG |
| 19 | 1142034 | 1142118 | Ser | TGA |
| 20 | 1175863 | 1175944 | Leu | TAG |
| 21 | 1230028 | 1229942 | Ser | CGA |
| 22 | 1137462 | 1137389 | Val | GAC |
| 23 | 1030603 | 1030533 | Cys | GCA |
| 24 | 1000022 | 999949 | His | GTG |
| 25 | 961607 | 961536 | Gly | GCC |
| 26 | 807413 | 807341 | Arg | TCT |
| 27 | 786780 | 786708 | Thr | CGT |
| 28 | 715971 | 715889 | Leu | TAA |
| 29 | 708441 | 708354 | Ser | GCT |
| 30 | 680259 | 680178 | Leu | GAG |
| 31 | 631445 | 631373 | Phe | GAA |
| 32 | 626987 | 626901 | Ser | GGA |
| 33 | 293477 | 293405 | Thr | TGT |
| 34 | 293399 | 293317 | Tyr | GTA |
| 35 | 269142 | 269070 | Ala | TGC |
| 36 | 269065 | 268992 | Ile | GAT |
| 37 | 164389 | 164318 | Asn | GTT |
| 38 | 87522 | 87450 | Met | CAT |

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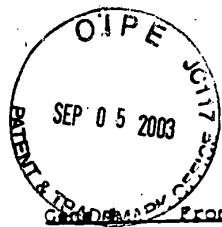


TABLE 2

| Gene | From | To | Strand | Gene function (C. trachomatis ortholog in parentheses) |
|---------|-------|-------|--------|--|
| CPn0001 | 282 | 4 | R | CT001 hypothetical protein |
| CPn0002 | 573 | 875 | F | gatC-Glu-tRNA Gln Amidotransferase (C subunit)-(CT002) |
| CPn0003 | 895 | 2370 | F | gatA-Glu tRNA Gln Amidotransferase-(CT003) |
| CPn0004 | 2170 | 3011 | F | gatB-(Pct112) Glu tRNA Gln Amidotransferase (B subunit)-(CT004) |
| CPn0005 | 4127 | 6892 | F | pmp_1-Polymorphic Outer Membrane Protein G Family |
| CPn0006 | 7293 | 7141 | R | |
| CPn0007 | 7605 | 10496 | F | |
| CPn0008 | 10975 | 11685 | F | |
| CPn0009 | 11815 | 13119 | F | |
| CPn0010 | 13435 | 14325 | F | |
| CPn0010 | 14379 | 15746 | F | frame-shift with 0010 |
| CPn0011 | 15892 | 16614 | F | |
| CPn0012 | 16644 | 18212 | F | |
| CPn0013 | 18584 | 21106 | F | pmp_2-Polymorphic Outer Membrane Protein G Family |
| CPn0014 | 21392 | 21922 | F | pmp_3-Polymorphic Outer Membrane Protein G Family |
| CPn0015 | 21835 | 24174 | F | pmp_3-PMP_3 (frame-shift with 0014) |
| CPn0016 | 24416 | 26188 | F | pmp_4-Polymorphic Outer Membrane Protein G Family |
| CPn0017 | 26094 | 27170 | F | pmp_4-PMP_4 (frame-shift with 0016) |
| CPn0018 | 27522 | 29003 | F | pmp_5-Polymorphic Outer Membrane Protein G Family |
| CPn0019 | 29007 | 30356 | F | pmp_5-PMP_5 (frame-shift with 0018) |
| CPn0020 | 32687 | 30603 | R | Predicted OMP [leader (14) peptide: outer membrane]-(CT351) |
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| CPn0022 | 34982 | 34395 | R | maf-(CT349) |
| CPn0023 | 36603 | 35014 | R | yjjK/alr-ABC Transporter Protein ATPase-(CT348) |
| CPn0024 | 37596 | 36661 | F | xerC-Integrase/recombinase-(CT347) |
| CPn0025 | 38604 | 37684 | R | elac/atsA-Sulphohydrolase/Glycosulfatase-(CT346) |
| CPn0026 | 39625 | 38762 | R | CT345 hypothetical protein-(CT345) |
| CPn0027 | 42234 | 39778 | R | lon-Lon ATP-dependent Protease-(CT344) |
| CPn0028 | 43325 | 42543 | R | |
| CPn0029 | 43755 | 43390 | R | |
| CPn0030 | 43891 | 44529 | F | gcp_1-O-Sialoglycoprotein Endopeptidase_1-(CT343) |
| CPn0031 | 44711 | 44884 | F | rs21-S21 Ribosomal Protein-(CT342) |
| CPn0032 | 44923 | 46098 | F | dnaJ-Heat Shock Protein J-(CT341) |
| CPn0033 | 46138 | 48171 | F | pdhA&B/odhA&odhB-(pyruvate) Oxoisovalerate Dehydrogenase Alpha & Beta Fusion-(CT340) |
| CPn0034 | 49457 | 48210 | R | |
| CPn0035 | 51029 | 49569 | R | CT339 hypothetical protein |
| CPn0036 | 51002 | 51796 | F | CT338 hypothetical protein |
| CPn0037 | 51792 | 52115 | F | ptsH-PTS Phosphocarrier Protein Hpr-(CT337) |
| CPn0038 | 52119 | 53831 | F | ptsI-PTS PEP Phosphotransferase-(CT336) |
| CPn0039 | 54250 | 53963 | R | ybaB-(CT335) |
| CPn0040 | 55643 | 54318 | R | dnaX_1-DNA Pol III Gamma and Tau_1-(CT334) |
| CPn0041 | 55996 | 57342 | F | |
| CPn0042 | 57403 | 58182 | F | |
| CPn0043 | 58447 | 60372 | F | |
| CPn0044 | 60419 | 60778 | F | |
| CPn0045 | 61069 | 62790 | F | |
| CPn0046 | 62790 | 63263 | F | |
| CPn0047 | 63455 | 63652 | F | |
| CPn0048 | 63687 | 65801 | F | *yqfP-Bs conserved hypothetical IM protein |
| CPn0049 | 66296 | 65817 | R | |
| CPn0050 | 66813 | 66499 | R | |
| CPn0051 | 66833 | 67111 | F | |
| CPn0052 | 68005 | 67304 | R | hemC-Porphobilinogen Deaminase-(CT299) |
| CPn0053 | 69344 | 67986 | R | sms-Sms Protein-(CT298) |
| CPn0054 | 70023 | 69313 | R | rnc-Ribonuclease III-(CT297) |
| CPn0055 | 70129 | 70590 | F | CT296 hypothetical protein |
| CPn0056 | 70953 | 72746 | F | mrsA-Phosphomannomutase-(CT295) |
| CPn0057 | 72934 | 73554 | F | sodM-Superoxide Dismutase (Mn)-(CT294) |
| CPn0058 | 73639 | 74562 | F | accD-AcCoA Carboxylase/Transferase Beta-(CT293) |
| CPn0059 | 74616 | 75050 | F | dut-dUTP Nucleotidohydrolase-(CT292) |
| CPn0060 | 75055 | 75528 | F | ptsN_1-PTS IIA Protein-(CT291) |
| CPn0061 | 75534 | 76208 | F | ptsN_2-PTS IIA Protein + HTH DNA-Binding Domain-(CT290) |
| CPn0062 | 76308 | 77690 | F | CT289 hypothetical protein |
| CPn0063 | 78112 | 78267 | F | |
| CPn0064 | 78346 | 78576 | F | |
| CPn0065 | 78924 | 80651 | F | CT288 hypothetical protein |
| CPn0066 | 80925 | 82655 | F | |

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